# Multidimensional scaling reveals the main evolutionary pathways of class A G-protein-coupled receptors



| | |
|---|---|
| Titre | Multidimensional scaling reveals the main evolutionary pathways of class A G-protein-coupled receptors |
| Type de publication | Article de revue |
| Auteur | Pele, J. [1], Abdi, H. [2], Moreau, Matthieu [3], Thybert, D. [4], Chabbert, Marie [5] |
| Editeur | Public Library of Science |
| Type | Article scientifique dans une revue à comité de lecture |
| Année | 2011 |
| Langue | Anglais |
| Date | 2011 |
| Numéro | 4 |
| Volume | 6 |
| Titre de la revue | PLoS One |
| ISSN | 1932-6203 |
| Mots-clés | Evolution, Molecular [6], Humans [7], Receptors, G-Protein-Coupled/classification/genetics [8] |
| Résumé en anglais | Class A G-protein-coupled receptors (GPCRs) constitute the largest family of transmembrane receptors in the human genome. Understanding the mechanisms which drove the evolution of such a large family would help understand the specificity of each GPCR sub-family with applications to drug design. To gain evolutionary information on class A GPCRs, we explored their sequence space by metric multidimensional scaling analysis (MDS). Three-dimensional mapping of human sequences shows a non-uniform distribution of GPCRs, organized in clusters that lay along four privileged directions. To interpret these directions, we projected supplementary sequences from different species onto the human space used as a reference. With this technique, we can easily monitor the evolutionary drift of several GPCR sub-families from cnidarians to humans. Results support a model of radiative evolution of class A GPCRs from a central node formed by peptide receptors. The privileged directions obtained from the MDS analysis are interpretable in terms of three main evolutionary pathways related to specific sequence determinants. The first pathway was initiated by a deletion in transmembrane helix 2 (TM2) and led to three sub-families by divergent evolution. The second pathway corresponds to the differentiation of the amine receptors. The third pathway corresponds to parallel evolution of several sub-families in relation with a covarion process involving proline residues in TM2 and TM5. As exemplified with GPCRs, the MDS projection technique is an important tool to compare orthologous sequence sets and to help decipher the mutational events that drove the evolution of protein families. |
| URL de la notice | http://okina.univ-angers.fr/publications/ua8334 [9] |
| DOI | 10.1371/journal.pone.0019094 [10] |

| | |
|---|---|
| Lien vers le document | http://dx.doi.org/10.1371/journal.pone.0019094 [10] |
| Titre abrégé | PLoS One |

**Liens**
[1] http://okina.univ-angers.fr/publications?f[author]=13612
[2] http://okina.univ-angers.fr/publications?f[author]=13614
[3] http://okina.univ-angers.fr/publications?f[author]=13685
[4] http://okina.univ-angers.fr/publications?f[author]=14398
[5] http://okina.univ-angers.fr/marie.chabbert/publications
[6] http://okina.univ-angers.fr/publications?f[keyword]=8725
[7] http://okina.univ-angers.fr/publications?f[keyword]=991
[8] http://okina.univ-angers.fr/publications?f[keyword]=13632
[9] http://okina.univ-angers.fr/publications/ua8334
[10] http://dx.doi.org/10.1371/journal.pone.0019094